

## SEQUENCE LISTING

110> Guerin-Marchand, Claudine Druilhe, Pierre

- <120> Peptide Sequences Specific for the Hepatic Stages of P. Falciparum Bearing Epitopes Capable of Stimulating the T Lymphocytes
- <130> 010830-118
- <140> US 09/900,963
- <141> 2001-07-10
- <150> US 08/098,327
- <151> 1993-11-24
- <150> PCT/FR92/00104
- <151> 1992-02-05
- <150> FR 91 01286
- <151> 1991-02-05
- <160> 47
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Xaa

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Xaa

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Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser
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Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile
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Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val Glu
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Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp Gly
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Leu Tyr Gly Arg Leu Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn
                            40
Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn
                        55
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Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr
                    70
                                        75
Asn Arg Glu Ser Ile Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His
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Lys Gly His Leu Glu Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln
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Lys Glu Asp Lys Ser
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Glu Ser Ile Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys
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Phe Asn Ser Leu Val Lys Ser Val Gln Gln Gln Gln His Asn Val
                            40
                                                45
Glu Glu Lys Val Glu Glu Ser Val Glu Glu Asn Asp Glu Glu Ser Val
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                                            60
Glu Glu Asn Val Glu Glu Asn Val Glu Glu Asn Asp Asp Gly Ser Val
                    70
                                        75
Ala Ser Ser Val Glu Glu Ser Ile Ala Ser Ser Val Asp Glu Ser Ile
                                    90
Asp Ser Ser Ile Glu Glu Asn Val Ala Pro Thr Val Glu Glu Ile Val
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Ala Pro Thr Val Glu Glu Ile Val Ala Pro Ser Val Val Glu Lys Cys
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Ala Pro Ser Val Glu Glu Ser Val Ala Pro Ser Val Glu Glu Ser Val
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Ala Glu Met Leu Lys Glu Arg
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Phe Asn Ser Leu Val Lys Ser Val Gln Gln Gln Gln His Asn
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Val Lys Glu Asn Ile Leu Glu Glu Ser Gln
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Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu
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Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
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Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys
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Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
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Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
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Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg
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Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
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Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Arg Asp Leu Glu
                            200
                                                 205
        195
Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His
                        215
                                             220
Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro Ala
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Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu
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Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val
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agagacttgc taaagaaaag ttgcaagaac aacaaagcga tctagaacaa gagagacgtg 180
ctaaagaaaa gttgcaagaa caacaaagcg atttagaaca agagagacgt gctaaagaaa 240
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atagagaatc tattacaaca aatgttgaag gacgaaggga tatacataaa ggacatcttg 900
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aqtqttcaac aaqaacaaca acacaatqtt qaaqaaaaag ttgaagaaag tgtagaagaa 180
aatqacqaaq aaaqtqtaqa aqaaaatqta qaaqaaaatg tagaagaaaa tgacgacgga 240
agtgtagcct caagtgttga agaaagtata gcttcaagtg ttgatgaaag tatagattca 300
agtattqaaq aaaatqtaqc tccaactqtt qaaqaaatcq tagctccaac tgttgaagaa 360
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  aaaaagatga aatcataaaa totaacttga gaagtggtto ttoaaattot aggaatcgaa 180
  taaatgagga aaatcacgag aagaaacacg ttttatctca taattcatat gagaaaacta 240
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  aaaatgtgtc acaaacaaat ttcaaaagtc ttttaagaaa tcttggtgtt tcagagaata 360
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  aaagcgattt agaacaagag agacgtgcta aagaaaagtt gcaagaacaa caaagcgatt 780
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  ttg ata ttt cat ata aat gga aag ata ata aag aat tct gaa aaa gat
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														agg Arg		144
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tca Ser 65	tat Tyr	gag Glu	aaa Lys	act Thr	aaa Lys 70	aat Asn	aat Asn	gaa Glu	aat Asn	aat Asn 75	aaa Lys	ttt Phe	ttc Phe	gat Asp	aag Lys 80	240
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ttc Phe	aaa Lys	agt Ser	ctt Leu 100	tta Leu	aga Arg	aat Asn	ctt Leu	ggt Gly 105	gtt Val	tca Ser	gag Glu	aat Asn	ata Ile 110	ttc Phe	ctt Leu	336
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gaa Glu	caa Gln	caa Gln	agc Ser 180	gat Asp	tta Leu	gaa Glu	caa Gln	gag Glu 185	aga Arg	ctt Leu	gct Ala	aaa Lys	gaa Glu 190	aag Lys	ttg Leu	576
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														aaa Lys		672
aag Lys 225	ttg Leu	caa Gln	gaa Glu	caa Gln	caa Gln 230	agc Ser	gat Asp	tta Leu	gaa Glu	caa Gln 235	gag Glu	aga Arg	cgt Arg	gct Ala	aaa Lys 240	720
gaa Glu	aag Lys	ttg Leu	caa Gln	gaa Glu 245	caa Gln	caa Gln	agc Ser	gat Asp	tta Leu 250	gaa Glu	caa Gln	gag Glu	aga Arg	cgt Arg 255	gct Ala	768

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Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
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                                                                   912
ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag
Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
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Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn
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Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn
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Phe Lys Ser Leu Leu Arg Asn Leu Gly Val Ser Glu Asn Ile Phe Leu
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Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys
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        275
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                                 25
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Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
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                                    315
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Gln 145	Glu	Arg	Leu	Ala	Lys 150	Glu	Lys	Leu	Gln	Glu 155	Gln	Gln	Ser	Asp	Leu 160
	Gln	Glu	Arg	Arg 165		Lys	Glu	Lys	Leu 170		Glu	Gln	Gln	Ser 175	Asp
			180					185					190	Gln	
		195					200					205		Gln	
_	210				_	215		_			220			Glu	
225	_			_	230					235				Arg	240
				245					250					Tyr 255	
			260					265					270	Ser	
		275					280					285		Ser -	
	290				-	295	_	_			300	_		Leu -	
305					310					315				Lys	320
	_			325					330					Asp 335	
			340					345					350	Glu	
•	•	355			•		360			_		365		Asp	
	370					375					380			Asn	
385					390					395				Asn	400
_	_		_	405	-				410					Ser 415	
	_		420					425					430	Asn	
		435					440					445		Lys -	
-	450	•	-			455	_		_		460			Lys	
465					470					475				Val	480
Glu	Leu	Ser	Glu	Asp 485	Ile	Thr	Lys	Tyr	Phe 490	Met	Lys	Leu	Lys	Val 495	île
Tyr															

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